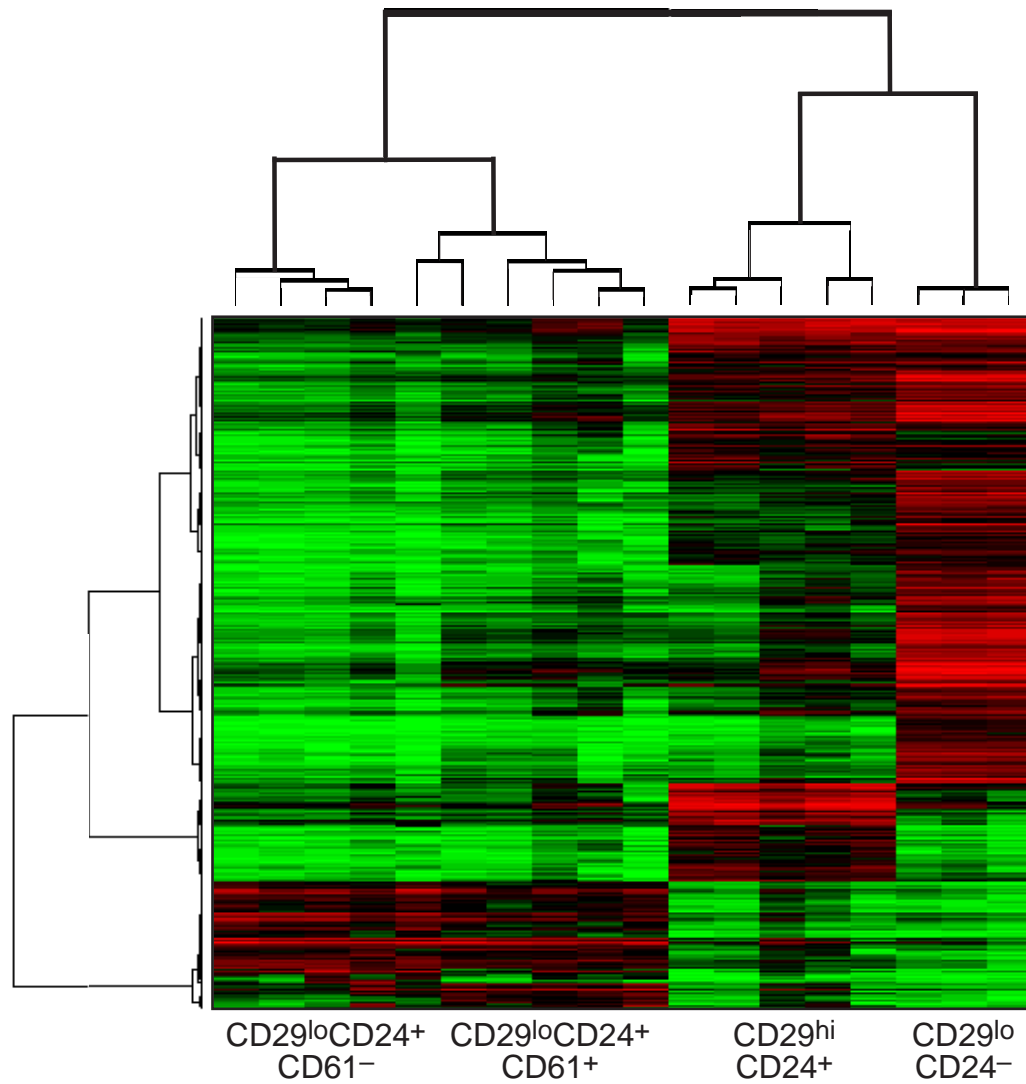
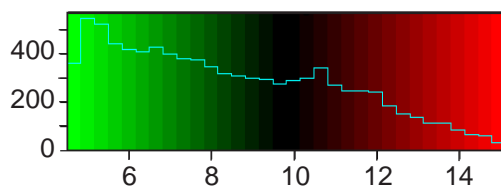


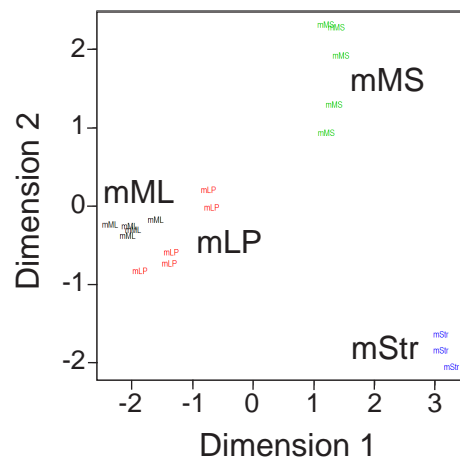
(a)



(b)



(c)



**Supplementary Figure 2. The mouse mammary cell subpopulations defined by CD24, CD29 and CD61 have distinct gene expression profiles. (a)** Hierarchical clustering and heatmap of the 500 genes most variable between the MaSC-enriched (CD29<sup>hi</sup>CD24<sup>+</sup>), luminal progenitor (CD29<sup>lo</sup>CD24<sup>+</sup>CD61<sup>+</sup>), mature luminal (CD29<sup>lo</sup>CD24<sup>+</sup>CD61<sup>-</sup>), and stromal (CD29<sup>lo</sup>CD24<sup>-</sup>) mammary cell subpopulations. **(b)** Color key and histogram of log-expression of genes in the heatmap. **(c)** Multidimension scaling plot showing clear separation of the MaSC-enriched (mMS), luminal progenitor (mLP), mature luminal (mML) and stromal (mStr) cell subpopulations.